through 585) are disclosed as encoding both a maize or soybean glutamate tRNA ligase enzyme or fragment thereof and a maize or soybean glutamyl-tRNA reductase enzyme of fragment thereof. Furthermore, SEQ ID NOs: 290 through 306 and 586 through 609 are erroneously associated with encoding a maize or soybean Mg-chelatase enzyme or fragment thereof. A similar typographical error is apparent with respect to the assertion at page 32, lines 1-2, the SEQ ID NOs: 95 and 96 encode a maize or soybean protochlorophyllide reductase enzyme or fragment thereof. Support for the amendments to the specification, as well as the correct association or SEQ ID NOs encoding their respective enzymes, can be found, for example, at page 66, line 17 through page 67, line 23 and in Table A. No new matter enters by these amendments.

1. Rejection of Claims 11-21 under 35 U.S.C. § 101

Claims 11-21 have been erroneously rejected under 35 U.S.C. § 101 for allegedly not being supported "by either specific and/or substantial utility or a well established utility". Office Action mailed August 14, 2002 (Paper Number 24) ("Office Action"), at page 2. The Examiner acknowledges that Applicants have disclosed several utilities for the nucleic acid molecules of the present invention, however, the Examiner contends that none of the utilities disclosed in the present application satisfy 35 U.S.C. § 101 because they are "applicable to any nucleic acids in general". Office Action at page 3.

As Applicants have previously stated, the "basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility...where specific benefit exists in currently available form." *Brenner v. Manson*, 383 U.S. 519, 534-35, 148 U.S.P.Q. 689, 695 (1966). Applicants have met this part of the bargain – they have disclosed nucleic acid molecules which, in their current form, provide at least one specific benefit to the public, for example use to identify a polymorphism in a population of maize plants. This benefit is specific, not vague or unknown, and it is a "real world" or substantial benefit.

The "threshold for utility is not high: An invention is 'useful' under section 101 if it is capable of providing some identifiable benefit." *Juicy Whip, Inc. v. Orange Bang,*

Inc., 185 F.3d 1364, 1366, 51 U.S.P.Q.2d 1700, 1702 (Fed. Cir. 1999), *citing Brenner v. Manson*, 383 U.S. 519, 534 (1966). Furthermore, an invention need only provide one identifiable benefit to satisfy 35 U.S.C. § 101. *See Raytheon Co. v. Roper Corp.*, 724 F.2d 951, 958, 220 U.S.P.Q. 592, 598 (Fed. Cir. 1983) ("when a properly claimed invention meets at least one stated objective, utility under section 101 is clearly shown").

The courts have expressed a test for utility that hinges on whether an invention provides an "identifiable benefit." *Juicy Whip, Inc. v. Orange Bang, Inc.*, 185 F.3d 1364, 1366, 51 U.S.P.Q.2d 1700, 1702 (Fed. Cir. 1999), *citing Brenner v. Manson*, 383 U.S. 519, 534 (1966). For analytical purposes, the requirement for an "identifiable benefit" may be broken into two prongs: (1) the invention must have a specific, *i.e.*, not vague or unknown benefit, *In re Brana*, 51 F.3d 1560, 1565, 34 U.S.P.Q.2d 1436, 1440 (Fed. Cir. 1995); and (2) the invention must provide a real world, *i.e.*, practical or "substantial" benefit. *Fujikawa v. Wattanasin*, 93 F.3d 1559, 1563, 39 U.S.P.Q.2d 1895, 1899 (Fed. Cir. 1996). A corollary to this test for utility is that the invention must not be "totally incapable of achieving a useful result," *i.e.*, the utility must not be incredible or unbelievable. *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571, 24 U.S.P.Q.2d 1401, 1412 (Fed. Cir. 1992).

The present specification discloses several uses for the claimed nucleic acid molecules, including use a nucleic acid molecule markers and probes (*see, e.g.*, specification at page 68, line 17 through page 69, line 9); to identify and obtain nucleic acid homologues (*see, e.g.*, specification at page 80, line 8 through page 81, line 9); to identify the presence or absence of a polymorphism (*see, e.g.*, specification at page 83, line 9 through page 91, line 3); to identify the concentration, presence or expression pattern of mRNA in a sample (*see, e.g.*, specification at page 96, line 14 through page 97, line 23); use to transform plants and other organisms (*see, e.g.*, specification at page 108, line 6 thorough page 118, line 9); and use to overexpress or suppress a desired protein (*see, e.g.*, specification at page 126, line 17 through page 129, line 8).

The Examiner denigrates these utilities by claiming they are not "useful" because they are "applicable to any nucleic acids in general by the virtue of their inherent

property". Office Action at page 3. This is not correct. The claimed nucleic acid molecules are particularly useful, for example, to isolate a promoter active in the tetrapyrrole pathway of a maize or soybean plant. *See, e.g.,* specification at page 168, line 17 through page 238, line 9 (Example 1), and Table A. Furthermore, because each of the claimed nucleic acid molecules has been asserted in the specification to encode a maize glutamyl-tRNA reductase ("GluTR") or fragment thereof, use of the claimed nucleic acid molecules have particular relevance, for example, to the identification of polymorphisms, promoters, and patterns of expression of this enzyme. Furthermore, since GluTR is the rate limiting step in 5-aminolevulinic acid ("ALA") formation, the nucleic acid molecules of the present invention also have particular relevance to the tetrapyrrole pathway. *See, e.g.,* specification at page 2, line 21 through page 4, line 23.

Despite Applicants' disclosure, the Examiner maintains that "Applicants have not given any immediately apparent benefit (substantial utility) for the artisan to use the claimed nucleic acids for detection of polymorphisms over any other nucleic acids isolated from soybean or maize." Office Action at pages 5-6. In short, the Examiner appears to be arguing that the disclosed utilities are not legal utilities simply because other molecules can be used for the same purpose. That position is wrong as a matter of law – there is no requirement of exclusive utility in the patent law. *See Carl Zeiss Stiftung v. Renishaw PLC*, 945 F.2d 1173, 1180, 20 U.S.P.Q.2d 1094, 1100 (Fed. Cir. 1991) ("An invention need not be the best or the only way to accomplish a certain result..."). Such an argument would imply that a new golf club has no legal utility because other golf clubs can be used for the same purpose, *i.e.*, hitting golf balls. That position must be rejected as it requires reading "into the patent laws limitations and conditions which the legislature has not expressed," a practice condemned by the Supreme Court. *See Diamond v. Chakrabarty*, 447 U.S. 303, 308, 206 U.S.P.Q. 193, 196 (1980), *quoting United States v. Dubilier Condenser Corp.*, 289 U.S. 178, 199, 17 U.S.P.Q. 154, 162 (1933).

Moreover, it is factually incorrect that this use is not "specific" to the claimed nucleic acids. The claimed nucleic acid molecules provide, for example, a particularly appropriate and demonstrably useful starting point for a walk to isolate a promoter that is active in the tetrapyrrole pathway of a maize plant. Specification at page 82, line 5 through page 83, line 8. A random nucleic acid molecule does not provide an equally good starting point to isolate such a promoter. Furthermore, even if a random nucleic acid molecule provided a better starting point than the claimed nucleic acid molecules, it would not obviate the utility of the claimed nucleic acid molecules. An invention may be "less effective than existing devices but nevertheless meet the statutory criteria for patentability." *Custom Accessories, Inc. v. Jeffrey-Allan Indus.*, 807 F.2d 955, 960 n.12, 1 U.S.P.Q.2d 1196, 1199 n.12 (Fed. Cir. 1986).

The Examiner further argues that the "Applicants have not provided any convincing evidence other than references that indicate the general nature in comparative sequencing in investigating the structure and function of a molecule." Office Action at page 7. In support of this proposition, the Examiner relies on Iyer *et al.* (*Genome Biology*, 2001, vol. 2, no. 12). In response, Applicants contend that this article is best directed to the controversy in the art in general over prediction of function based on homology alone. Moreover, this article is directed to six examples that are unlike Applicants' present disclosure. For example, in each of the situations examined in Iyer *et al.* each orthologous gene sought was known to be either not well conserved among species (*e.g.*, there is a relatively low sequence similarity among various species) or the protein/amino acid sequence encoded by the orthologous gene was distantly related or unrelated to the protein from the original organism.

In contrast, Applicants' disclosure teaches that the deducted amino acid sequence of GluTR from all species exhibits about 60% overall similarity with stretches of amino acid identity. More specifically, for example, barley, *Arabidopsis* and cucumber show over 70% identity at the deducted amino acid level. *See* specification at page 5. The specification also teaches that the purified barley GluTR has a molecular weight of 270 kD with a monomeric subunit size of 54 kD. *Id.* at 4. Finally, Table A discloses that each of SEQ ID NOs 586, 590, 594, 596, 597, 599, 600, 604, and 605 exhibits a high

sequence similarity with a maize glutamyl-tRNA reductase, ranging from about 82% to about 89% sequence identity. The Examiner has presented no evidence to suggest that one skilled in the art would doubt that the claimed nucleic acid molecules would encode a maize glutamyl-tRNA reductase enzyme.

Applicants have disclosed several specific, substantial and credible utilities for the claimed nucleic acid molecules. Any one of these utilities is enough to satisfy the requirements of 35 U.S.C. § 101. Because Applicants need only establish a single utility to satisfy 35 U.S.C. § 101, and have done so in the present case, the rejection under Section 101 is incorrect and should be reversed. Reconsideration and withdrawal of this rejection is respectfully requested.

2. Rejection of Claims 11-21 under 35 U.S.C. §112, 1st Paragraph: Enablement

Claims 11-21 were erroneously rejected as not enabled by the specification, because the claimed nucleic acid molecules allegedly lack utility and therefore cannot be enabled. Office Action at pages 7-8. This rejection is erroneous and has been overcome by the arguments stated above regarding utility because it is well-established law that "the enablement requirement is met if the description enables any mode of making and using the invention." *Johns Hopkins University v. CellPro*, 152 F.3d 1342, 1361, 47 U.S.P.Q.2d 1705, 1719 (Fed. Cir. 1998) (emphasis added), *quoting Engel Indus. v. Lockformer Co.*, 946 F.2d 1528, 1533, 20 U.S.P.Q.2d 1300, 1304 (Fed. Cir. 1991). Unless and until the Examiner comes forth with evidence to rebut the objective truth of the utilities disclosed in the specification, this enablement rejection must be withdrawn as improper. *See In re Wright*, 999 F.2d 1557, 1561-62, 27 U.S.P.Q.2d 1510, 1513 (Fed. Cir. 1993); *Ex parte Lemak*, 210 U.S.P.Q. 306, 307 (Bd. App. 1981) ("pure conjecture" does not substantiate rejection for lack of enablement).

Therefore, the rejection of claims 11-21 Under 35 U.S.C. § 112, first paragraph, is improper. Reconsideration and withdrawal of this rejection is respectfully requested.

3. Rejection of Claims 1, 2 and 10 under 35 U.S.C. §112, 1st Paragraph: Enablement

Claims 1, 2, and 10 also stand erroneously rejected under 35 USC § 112, first paragraph as allegedly containing subject matter which was not described in the specification in such a way as to enable on of skill in the art to make and/or use the invention. Office Action at pages 8-9.

Applicants maintain that the Examiner has not met the evidentiary burden to impose an enablement rejection for failure to enable one of skill to use the invention. A specification that discloses how to use a claimed invention "must be taken as in compliance with the enabling requirement of the first paragraph of § 112 unless there is reason to doubt the objective truth of the statements contained therein." *In re Brana*, 51 F.3d 1560, 1566, 34 U.S.P.Q.2d 1436, 1441 (Fed. Cir. 1995) (*quoting In re Marzocchi*, 439 F.2d 220, 223, 169 U.S.P.Q. 367, 369 (C.C.P.A. 1971) (emphasis in original)). It is also well-established that "the enablement requirement is met if the description enables any mode of making and using the invention." *Johns Hopkins University v. CellPro*, 152 F.3d 1342, 1361, 47 U.S.P.Q.2d 1705, 1719 (Fed. Cir. 1998) (emphasis added) (*quoting Engel Indus. v. Lockformer Co.*, 946 F.2d 1528, 1533, 20 U.S.P.Q.2d 1300, 1304 (Fed. Cir. 1991)).

The present specification teaches how to use the claimed invention as discussed *supra* in the section regarding utility. The Office Action has failed to provide specific evidence supporting this rejection, nor any specific explanation of why the specification allegedly fails to enable these uses. *See In re Wright*, 999 F.2d 1557, 1561-62, 27 USPQ2d 1510, 1513 (Fed. Cir. 1993); *Ex parte Lemak*, 210 USPQ 306, 307 (Bd. App. 1981) ("pure conjecture" does not substantiate rejection for lack of enablement). For at least this reason, withdrawal of this rejection is respectfully requested.

The Examiner asserts "if the claimed nucleic acids do not encode a Glu TR, no matter how routine the experimentation might be, the nucleic acids cannot be used as the claims intended purpose." Office Action at page 8. To support this proposition, the Office Action argues that homology is not sufficient to assign protein function and relies on Iyer *et al.* for support. *Id.* at page 9.

Applicants reiterate the arguments discussed *supra* with respect to the differences between the orthologous genes discussed in Iyer *et al.* and Applicants' disclosure. Furthermore, Applicants reiterate that the Examiner has presented no evidence to suggest that one skilled in the art would doubt that the claimed nucleic acid molecules would encode a maize glutamyl-tRNA reductase enzyme based on the present disclosure. Rather, the Examiner contends that "Applicants have failed to give any evidence via example that the claimed nucleic acids indeed have this functionality." Office Action at page 9. This requisite goes beyond what is required by law. The specification need not contain an example if the invention is otherwise disclosed in such manner that one skilled in the art will be able to practice it without an undue amount of experimentation. *In re Borkowski*, 422 F.2d 904, 908, 164 U.S.P.Q. 642, 645 (C.C.P.A. 1970); MPEP § 2164.02 at 2100-176. Furthermore, Applicants need only show that one skilled in the art would be able to make and use the claimed invention using the application as a guide. *In re Brandstadter*, 484 F.2d 1395, 1406-07, 179 U.S.P.Q. 286, 294 (C.C.P.A. 1973). The evidence provided by applicant need not be conclusive but merely convincing to one skilled in the art. MPEP § 2164.05 at page 2100-179 (emphasis in original).

Accordingly, for at least the foregoing reasons, and the arguments made in Applicants' prior response, the rejection of claims 1, 2 and 10 under 35 U.S.C. § 112, first paragraph, is improper. Reconsideration and withdrawal of this rejection is respectfully requested.

4. Rejection of Claims 1, 2, 10 and 11 under 35 U.S.C. §112, 1st Paragraph: Written Description

Claims 1, 2, 10 and 11 have been erroneously rejected under 35 U.S.C. § 112, first paragraph, for allegedly not being described in the specification "in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." Office Action at page 9. The Examiner does not dispute that Applicants had possession of and have adequately described the claimed SEQ ID NOs. Office Action mailed February 1, 2001, at page 5. However, the Examiner argues that "[i]t would not be possible for the skilled artisan to

envision that Applicants had possession of [a full-length cDNA or a gene sequence] nor would it be within the purview of a skilled artisan to fabricate a full-length cDNA or gene sequence which 'comprise' the claimed nucleic acids based on the specification or the prior art." Office Action at page 10. The Examiner contends that the "presently claimed nucleic acids fail to meet the requirement because the specification fails to disclose a full open reading frame for each of the claimed SEQ ID Numbers. Therefore, a nucleic acid 'comprising' such SEQ ID Number would read on an undescribed region of a full-length cDNA as well as a gene sequence." Office Action at page 10.

This argument flies in the face of the existing patent jurisprudence. It is well-established law that use of the transitional term "comprising" leaves the claims "open for the inclusion of unspecified ingredients even in major amounts." *Ex parte Davis*, 80 U.S.P.Q. 448, 450 (B.P.A.I. 1948). *Accord PPG Indus. v. Guardian Indus.*, 156 F.3d 1351, 1354, 48 U.S.P.Q.2d 1351, 1353-54 (Fed. Cir. 1998); *Moleculon Research Corp. v. CBS*, 793 F.2d 1261, 1271, 229 U.S.P.Q. 805, 812 (Fed. Cir. 1986). The very nature of "unspecified ingredients" is that they are not specified or described. The Examiner attempts to turn the legal meaning of "comprising" on its head by requiring Applicants to describe hypothetical claim elements. Applicants need only describe the claimed invention, and they have done so in the present application.

Furthermore, as Applicants have previously stated, the purpose of the written description requirement is to ensure that the inventors had possession of the claimed subject matter, *i.e.*, to ensure that the inventors actually invented what is claimed. *Gentry Gallery Inc. v. Berkline Corp.*, 134 F.3d 1473, 1479, 45 U.S.P.Q.2d 1498, 1503 (Fed. Cir. 1998); *Lockwood v. American Airlines*, 107 F.3d 1565, 1572, 41 U.S.P.Q.2d 1961, 1966 (Fed. Cir. 1997); *In re Alton*, 76 F.3d 1168, 1172, 37 U.S.P.Q.2d 1578, 1581 (Fed. Cir. 1996). If a person of ordinary skill in the art would, after reading the specification, understand that the inventors had possession of the claimed invention, even if not every nuance, then the written description has been met. *In re Alton*, 76 F.3d at 1175, 37 U.S.P.Q.2d at 1584. A person of ordinary skill in the art, *e.g.*, a molecular biologist, would, after reading the present specification, understand that Applicants had possession

of nucleic acid molecules comprising nucleic acid sequences selected from the group of SEQ ID NOs: 586, 590, 594, 596, 597, 599, 600, 601, 604, 605, complements and variations thereof, as well as the enzymes they encode, and therefore, the claimed invention.

The Examiner acknowledges that Applicants have pointed out the specification teaches that the claimed nucleic acid molecules may include the recited sequence with additional sequences, for example, vectors comprising the claimed nucleic acid molecules (specification at page 36, line 7 through page 40, line 6, and at page 109, line 4 through page 118, line 9), and extra nucleotides or detectable labels added to the claimed nucleic acid sequences (specification at page 58, lines 19-24). *See* Office Action at page 10. The specification also describes, for example, nucleic acid molecules comprising nucleic acid sequences having conservative substitutions (specification at page 64, line 4 through page 65, line 19), fusion protein or peptide molecules or fragments thereof encoded by the nucleic acid molecules of the present invention (specification at page 75, lines 12-23), plant homologue proteins (specification at page 76, lines 1-14), site directed mutagenesis of the claimed nucleic acid molecules (specification at page 103, line 16 through page 105, line 7), references describing the construction, manipulation and isolation of nucleic acid macromolecules (specification 161, line 22 through page 162, line 6) and construction of cDNA libraries using the claimed nucleic acid molecules (specification at page 168, line 17 through page 238, line 20 (Examples 1-2)). Although the Examiner admits that these embodiments could very well be envisioned by a skilled artisan, the Examiner maintains that "[i]t would not be possible for the skilled artisan to envision that Applicants had possession of such molecules". Office Action at page 10.

The Examiner appears to assert that each nucleic acid molecule within a claimed genus must be described by its complete structure. Office Action at page 10. This assertion is unfounded. The Federal Circuit has elucidated a test for written description wherein a genus of nucleic acids may be described by a structural feature that distinguishes members of the claimed genus from non-members of the claimed genus. *Regents of the University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1568-69, 43

U.S.P.Q.2d 1398, 1406 (Fed. Cir. 1997). Applicants have satisfied that test for written description.

In particular, Applicants have disclosed common structural features, for example the nucleotide sequences of SEQ ID NO: 586, SEQ ID NO: 590, SEQ ID NO: 594, etc. The respective common structural feature (the nucleotide sequences of SEQ ID NOs: 586, 590, 594, 596, 597, 599, 600, 601, 604 and 605) is shared by every nucleic acid molecule in the claimed genera, and it distinguishes the members of the claimed genera from non-members. For example, if a nucleic acid molecule such as an mRNA contains the nucleotide sequence of SEQ ID NO: 586, then it is a member of the claimed genus of nucleic acid molecules comprising a nucleic acid sequence of SEQ ID NO: 586.[1] If a nucleic acid molecule does not contain SEQ ID NO: 586, then it is not a member of that claimed genus. The presence of other nucleotides at either end of the recited sequence will not interfere with the recognition of a claimed nucleic acid molecule as such – it either contains the nucleotides of SEQ ID NO: 586 or it does not.

In light of the detailed disclosure of the present application, one skilled in the art, after reading the present specification, would clearly know if a nucleic acid molecule contains one of the recited nucleotide sequences. Thus, claims 1, 2, 10 and 11 are supported by an adequate written description pursuant to the requirements of 35 U.S.C. § 112, and the rejection should be reversed. Reconsideration and reversal are respectfully requested.

5. The Rejection of Claim 1 Under 35 U.S.C. § 102

Claim 1 was erroneously rejected under 35 U.S.C. § 102(b) over Baysdorfer (GenBank accession number W21756, May 1996). According to the Examiner, "Baysdorfer discloses a cDNA sequence of Zea mays glutamyl-tRNA reductase that has

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[1] The same argument applies with equal force to every genus of the claimed nucleic acid molecules. For example, if a nucleic acid molecule such as an mRNA contains the nucleotide sequence of SEQ ID NO: 590, then it is a member of the claimed genus of nucleic acid molecules comprising a nucleic acid sequence of SEQ ID NO: 590. *See, e.g.*, claim 13.

an overall homology of 76.8% to SEQ ID Number 586, thus encoding a fragment of the claimed enzyme." Office Action at page 11.

This reference does not anticipate presently amended claim 1. For a prior art reference to anticipate in terms of 35 U.S.C. § 102, every element of the claimed invention must be identically shown in a single reference. *Diversitech Corp. v. Century Steps, Inc.*, 850 F.2d 675, 677, 7 U.S.P.Q. 2d 1315, 1317 (Fed. Cir. 1988). *See also Kalman v. Kimberly Clark Corp.*, 713 F.2d 760, 771 (Fed. Cir. 1983). Baysdorfer does not teach every element of the claimed invention.

Claim 1 has been amended to recite a substantially purified nucleic acid molecule that encodes a maize or soybean glutamyl-tRNA reductase enzyme or fragment thereof, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 586, 590, 594, 596, 597, 599, 600, 601, 604, 605 and complements thereof. Because the cited reference does teach the claimed sequences, it cannot anticipate the presently amended claims.

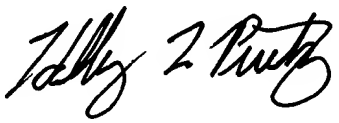
Thus, the rejection of claim 1 under 35 U.S.C. § 102(b) over Baysdorfer is improper. Reconsideration and withdrawal of this rejection are respectfully requested.

Conclusion

In view of the foregoing amendments and remarks, it is respectfully submitted that the present application is now in condition for allowance, and notice of such is respectfully requested. The Examiner is encouraged to contact the undersigned should any additional information be necessary for allowance.

In the event that extensions of time are necessary to prevent abandonment of this patent application, then such extensions of time are hereby petitioned. Applicants do not believe that any fees in addition to those provided for in the accompanying documents, are due at this time. However, if any fees under 37 C.F.R. §§ 1.16 or 1.17 are required in the present application, including any fees for extensions of time, then the Commissioner is hereby authorized to charge such fees to Deposit Account No. 50-2387, referencing docket number 16517.231.

Respectfully submitted,



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Marked-up Version of Amended Specification

At page 30, lines 1-18:

The present invention also provides a substantially purified maize or soybean glutamyl-tRNA reductase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: **[266]290** through SEQ ID NO: **[289]306** and SEQ ID NO: **[570]586** through SEQ ID NO: **[585]609**.

The present invention also provides a substantially purified maize or soybean glutamyl-tRNA reductase enzyme fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: **[266]290** through SEQ ID NO: **[289]306** and SEQ ID NO: **[570]586** through SEQ ID NO: **[585]609**.

The present invention also provides a substantially purified maize or soybean Mg-chelatase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of a complement of SEQ ID NO: **[290]307** through SEQ ID NO: **[306]371** and SEQ ID NO: **[586]610** through SEQ ID NO: **[609]652**.

The present invention also provides a substantially purified maize or soybean Mg-chelatase enzyme or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: **[290]307** through SEQ ID NO: **[306]371** and SEQ ID NO: **[586]610** through SEQ ID NO: **[609]652**.

At page 31, line 18 through page 32, line 2:

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to a maize or soybean protochlorophyllide reductase enzyme or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group

consisting of a complement of SEQ ID NO: 9 through SEQ ID NO: 94 and SEQ ID NO: 398 through SEQ ID NO: 466 or a nucleic acid sequence selected from the group consisting of SEQ ID NO: **[95]**9 through SEQ ID NO: **[96]**94 and SEQ ID NO: 398 through SEQ ID NO: 466.

Marked-up Version of Amended Claims

1. (Twice Amended) A substantially purified nucleic acid molecule that encodes a maize **[or soybean tetrapyrrole pathway enzyme or fragment thereof, wherein said maize or soybean tetapyrrole pathway enzyme is a]** glutamyl-tRNA reductase enzyme **or fragment thereof, wherein said nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 586, 590, 594, 596, 597, 599, 600, 601, 604, 605 and complements thereof**.

10. (Amended) The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a nucleic acid sequence having between 100% and 90% identity with a sequence selected from the group consisting of SEQ ID NOs: 586, 590, 594, 596, 597, 599, 600, 601, 604, **[and]** 605**, and complements thereof**.